



Third Corrected Sequence Listing 5-2002

SEQUENCE LISTING

<110> Haru, Yoshiki
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Amedeo, Paolo
Paszkowski, Jerzy

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ccg gat att gag cag aga aag gat agt gtt gaa gag tcg aca gat aag	687
Pro Asp Ile Glu Gln Arg Lys Asp Ser Val Glu Glu Ser Thr Asp Lys	
115 120 125	

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atc	aag	cct	ata	atg	tca	gcc	cga	agt	tac	agg	gca	ttg	ttt	aga	ggg	735
Ile	Lys	Pro	Ile	Met	Ser	Ala	Arg	Ser	Tyr	Arg	Ala	Leu	Phe	Arg	Gly	
130															140	
aag	ctc	aag	tct	gag	gca	tta	gtt	gat	gct	tcc	cca	aat	gaa	gag	783	
Lys	Leu	Lys	Glu	Ser	Glu	Ala	Leu	Val	Asp	Ala	Ser	Pro	Asn	Glu	Glu	
145															155	
gaa	cta	gta	gtt	gtt	ggt	tgt	tct	cgc	cgc	ata	cct	gca	ggc	aat	gat	831
Glu	Leu	Val	Val	Val	Gly	Cys	Ser	Arg	Arg	Ile	Pro	Ala	Gly	Asn	Asp	
160															170	
gat	gtt	caa	ggt	aaa	aca	gat	tgt	cca	cca	cct	gca	gat	gca	gga	tca	879
Asp	Val	Gln	Gly	Lys	Thr	Asp	Cys	Pro	Pro	Pro	Ala	Asp	Ala	Gly	Ser	
175															190	
aaa	agg	ctg	cca	gtt	gac	gaa	act	agt	ttg	gac	aag	ggc	act	gat	ttt	927
Lys	Arg	Leu	Pro	Val	Asp	Glu	Thr	Ser	Leu	Asp	Lys	Gly	Thr	Asp	Phe	
195															205	
cct	ttg	aaa	tca	gtt	acg	gag	acc	gag	aag	ata	gtg	ctt	gat	gca	tcc	975
Pro	Leu	Lys	Ser	Val	Thr	Glu	Thr	Glu	Lys	Ile	Val	Leu	Asp	Ala	Ser	
210															220	
ccc	ata	gtt	gaa	act	ggg	gat	gac	agt	gtt	ata	ggt	tca	cca	tct	gag	1023
Pro	Ile	Val	Glu	Thr	Gly	Asp	Asp	Ser	Val	Ile	Gly	Ser	Pro	Ser	Glu	
225															235	
aat	tta	gag	aca	caa	aag	ctt	caa	gat	ggt	aag	aca	gat	tgt	tca	cca	1071
Asn	Leu	Glu	Thr	Gln	Lys	Leu	Gln	Asp	Gly	Lys	Thr	Asp	Cys	Ser	Pro	
240															250	
cct	gca	aat	gca	gaa	tcg	aaa	acg	ctg	cca	gtt	ggt	gaa	act	agt	tta	1119
Pro	Ala	Asn	Ala	Glu	Ser	Lys	Thr	Leu	Pro	Val	Gly	Glu	Thr	Ser	Leu	
255															270	
gaa	aaa	gaa	tat	cca	caa	aag	ttt	caa	gat	gat	aac	aca	gat	tgt	cta	1167
Glu	Lys	Glu	Tyr	Pro	Gln	Lys	Phe	Gln	Asp	Asp	Asn	Thr	Asp	Cys	Leu	
275															285	
cca	cct	gca	aat	gca	gaa	tca	aaa	agg	ctg	cca	gtt	ggc	gaa	act	agt	1215
Pro	Pro	Ala	Asn	Ala	Glu	Ser	Lys	Arg	Leu	Pro	Val	Gly	Glu	Thr	Ser	
290															300	
tta	gaa	aag	gac	act	gat	ttt	cct	ttg	aaa	tca	act	acg	gag	act	gga	1263
Leu	Glu	Lys	Asp	Thr	Asp	Phe	Pro	Leu	Lys	Ser	Thr	Thr	Glu	Thr	Gly	
305															315	
aag	atg	gtt	ctt	tat	gca	tcc	ccc	ata	gtt	gaa	act	agg	gat	gac	agc	1311
Lys	Met	Val	Leu	Tyr	Ala	Ser	Pro	Ile	Val	Glu	Thr	Arg	Asp	Asp	Ser	
320															330	
gtt	ata	tgt	tca	cca	tct	aca	aat	tta	gaa	acc	caa	aag	ctt	ctt	gtc	1359
Val	Ile	Cys	Ser	Pro	Ser	Thr	Asn	Leu	Glu	Thr	Gln	Lys	Leu	Leu	Val	
335															345	
agt	aaa	act	ggc	tta	gaa	acc	gac	ata	gtt	ttg	cct	ttg	aaa	aga	aaa	1407
Ser	Lys	Thr	Gly	Leu	Glu	Thr	Asp	Ile	Val	Leu	Pro	Leu	Lys	Arg	Lys	
355															360	
aga	gac	act	gca	gaa	att	gag	ctg	gat	gca	tgt	gct	aca	gtt	gca	aat	1455
Arg	Asp	Thr	Ala	Glu	Ile	Glu	Leu	Asp	Ala	Cys	Ala	Thr	Val	Ala	Asn	
370															375	
															380	

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gga gat gat cac gtt atg agt tct gat ggg gtc att cca tct cca tct Gly Asp Asp His Val Met Ser Ser Asp Gly Val Ile Pro Ser Pro Ser 385 390 395	1503
ggt tgc aaa aat gat aat cga cct gaa atg tgc aac acg tgt aaa aaa Gly Cys Lys Asn Asp Asn Arg Pro Glu Met Cys Asn Thr Cys Lys Lys 400 405 410	1551
cgg caa aag gtc aac ggt gat tgt caa aat agg agt gtt tgc tcc tgc Arg Gln Lys Val Asn Gly Asp Cys Gln Asn Arg Ser Val Cys Ser Cys 415 420 425 430	1599
att gtc cag cca gtt gaa gaa tct gat aac gtg aca cag gat atg aaa Ile Val Gln Pro Val Glu Glu Ser Asp Asn Val Thr Gln Asp Met Lys 435 440 445	1647
gaa act gga cca gtt acg agc aga gaa tat gag gag aac ggg caa ata Glu Thr Gly Pro Val Thr Ser Arg Glu Tyr Glu Glu Asn Gly Gln Ile 450 455 460	1695
caa cat ggt aaa tca agt gat ccc aaa ttc tat tct tcg gtg tac cca Gln His Gly Lys Ser Ser Asp Pro Lys Phe Tyr Ser Ser Val Tyr Pro 465 470 475	1743
gag tat tgg gtt cct gtg cag cta tca gat gta cag ctg gag caa tac Glu Tyr Trp Val Pro Val Gln Leu Ser Asp Val Gln Leu Glu Gln Tyr 480 485 490	1791
tgt cag act ctc ttc tcc aaa tcc tta tct ctt tct tca ctt tcg aag Cys Gln Thr Leu Phe Ser Lys Ser Leu Ser Leu Ser Leu Ser Lys Lys 495 500 505 510	1839
att gat ctt gga gct cta gaa gaa act ctc aat tct gta aga aaa acc Ile Asp Leu Gly Ala Leu Glu Glu Thr Leu Asn Ser Val Arg Lys Thr 515 520 525	1887
tgt gac cat cca tac gtt atg gat gca tct ttg aaa caa ctg ctc acc Cys Asp His Pro Tyr Val Met Asp Ala Ser Leu Lys Gln Leu Leu Thr 530 535 540	1935
aag aat ctg gag ttg cat gaa atc ctg gat gta gaa att aaa gcg agc Lys Asn Leu Glu Leu His Glu Ile Leu Asp Val Glu Ile Lys Ala Ser 545 550 555	1983
ggg aaa ctt cac ctc ctt gat aaa atg ctt act cat ata aaa aag aat Gly Lys Leu His Leu Leu Asp Lys Met Leu Thr His Ile Lys Lys Asn 560 565 570	2031
ggt tta aaa gca gtt gtc ttc tac cag gca aca caa acc cct gaa ggg Gly Leu Lys Ala Val Val Phe Tyr Gln Ala Thr Gln Thr Pro Glu Gly 575 580 585 590	2079
ctt ctg ctt ggt aat att ctc gaa gat ttt gtg ggt caa aga ttt ggt Leu Leu Leu Gly Asn Ile Leu Glu Asp Phe Val Gly Gln Arg Phe Gly 595 600 605	2127
cca aaa tct tat gag cat ggg ata tat tcc tca aag aag aac tcc gct Pro Lys Ser Tyr Glu His Gly Ile Tyr Ser Ser Lys Lys Asn Ser Ala 610 615 620	2175
ata aac aat ttc aac aag gag agt caa tgc tgt gtt ctg ctg ttg gaa Ile Asn Asn Phe Asn Lys Glu Ser Gln Cys Cys Val Leu Leu Leu Glu	2223

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625

630

635

2271

aca cgt gcc tgc agt caa acc att aaa ctc ttg cga gct gat gcg ttt
 Thr Arg Ala Cys Ser Gln Thr Ile Lys Leu Leu Arg Ala Asp Ala Phe
 640 645 650

2319

att ctt ttt gga agc agc ttg aat cca tcg cat gat gtt aag cac gta
 Ile Leu Phe Gly Ser Ser Leu Asn Pro Ser His Asp Val Lys His Val
 655 660 665 670

2367

gag aag ata aaa atc gag tca tgt tct gaa aga act aag ata ttc cga
 Glu Lys Ile Lys Ile Glu Ser Cys Ser Glu Arg Thr Lys Ile Phe Arg
 675 680 685

2415

ttg tac tca gta tgt aca gtt gaa gaa aaa gcc ctg att ctg gct agg
 Leu Tyr Ser Val Cys Thr Val Glu Glu Lys Ala Leu Ile Leu Ala Arg
 690 695 700

2463

caa aat atg cgg caa aat aaa gct gta gag aac cta aac cgc tct ctc
 Gln Asn Met Arg Gln Asn Lys Ala Val Glu Asn Leu Asn Arg Ser Leu
 705 710 715

2511

acg cac gca ctg ctc atg tgg ggg gcg tca tac tta ttt gat aaa ctg
 Thr His Ala Leu Leu Met Trp Gly Ala Ser Tyr Leu Phe Asp Lys Leu
 720 725 730

2559

gat cat ttt cac agc agt gaa act cca gat tca gga gtt tca ttt gaa
 Asp His Phe His Ser Ser Glu Thr Pro Asp Ser Gly Val Ser Phe Glu
 735 740 745 750

2607

caa tct att atg gac ggc gtg att cat gaa ttc tcg tcc ata ctt tct
 Gln Ser Ile Met Asp Gly Val Ile His Glu Phe Ser Ser Ile Leu Ser
 755 760 765

2655

tcc aaa ggt gga gaa aat gaa gtc aag ctg tgt cta ctt ttg gag
 Ser Lys Gly Gly Glu Asn Glu Val Lys Leu Cys Leu Leu Leu Glu
 770 775 780

2703

gcc aag cat gct cag gga act tac agc agt gat tct act cta ttt ggt
 Ala Lys His Ala Gln Gly Thr Tyr Ser Ser Asp Ser Thr Leu Phe Gly
 785 790 795

2751

gaa gac cat att aag ttg tca gat gaa gag agt cca aat ata ttt tgg
 Glu Asp His Ile Lys Leu Ser Asp Glu Glu Ser Pro Asn Ile Phe Trp
 800 805 810

2799

tca aag ctg ttg ggg gga aaa aat cct atg tgg aaa tac cct tca gat
 Ser Lys Leu Leu Gly Gly Lys Asn Pro Met Trp Lys Tyr Pro Ser Asp
 815 820 825 830

2847

act ccc caa agg aat cga aaa cga gtt cag tat ttt gag ggt tct gaa
 Thr Pro Gln Arg Asn Arg Lys Arg Val Gln Tyr Phe Glu Gly Ser Glu
 835 840 845

2895

gcg agt ccc aaa act ggc gat ggt gga aat gca aag aag cga aag aag
 Ala Ser Pro Lys Thr Gly Asp Gly Gly Asn Ala Lys Lys Arg Lys Lys
 850 855 860

2943

gct tct gat gat gtc act gat ccc cgg gtc act gat ccg cca gta gat
 Ala Ser Asp Asp Val Thr Asp Pro Arg Val Thr Asp Pro Pro Val Asp
 865 870 875

2991

gat gat gaa aga aag gcc tct ggg aag gat cac atg ggg gct ttg gag

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Asp	Asp	Glu	Arg	Lys	Ala	Ser	Gly	Lys	Asp	His	Met	Gly	Ala	Leu	Glu
880					885					890					
tca	cca	aaa	gtc	ata	aca	ctc	cag	tca	tca	tgt	aaa	tct	tct	ggt	aca
Ser	Pro	Lys	Val	Ile	Thr	Leu	Gln	Ser	Ser	Cys	Lys	Ser	Ser	Gly	Thr
895					900					905					910
gat	ggt	aca	ttg	gat	gga	aat	gat	gct	ttt	ggc	ttg	tat	tct	atg	ggc
Asp	Gly	Thr	Leu	Asp	Gly	Asn	Asp	Ala	Phe	Gly	Leu	Tyr	Ser	Met	Gly
									920					925	
915															
agc	cat	atc	tct	gga	atc	cca	gag	gat	atg	tta	gct	agt	caa	gat	tgg
Ser	His	Ile	Ser	Gly	Ile	Pro	Glu	Asp	Met	Leu	Ala	Ser	Gln	Asp	Trp
									935					940	
930															
ggt	aaa	ata	ccg	gat	gaa	tca	cag	agg	agg	ctc	cac	act	gtt	tta	aag
Gly	Lys	Ile	Pro	Asp	Glu	Ser	Gln	Arg	Arg	Leu	His	Thr	Val	Leu	Lys
									950					955	
945															
ccg	aag	atg	gca	aaa	ctt	tgc	caa	gtt	ttg	cat	ctt	tca	gat	gct	tgc
Pro	Lys	Met	Ala	Lys	Leu	Cys	Gln	Val	Leu	His	Leu	Ser	Asp	Ala	Cys
									965					970	
960															
aca	agc	atg	gtc	gga	aat	ttt	ctc	gaa	tat	gtt	att	gaa	aat	cac	cga
Thr	Ser	Met	Val	Gly	Asn	Phe	Leu	Glu	Tyr	Val	Ile	Glu	Asn	His	Arg
									980					990	
975															
atc	tac	gaa	gag	cca	gcc	act	act	ttt	cag	gca	ttc	cag	ata	gcc	ctg
Ile	Tyr	Glu	Glu	Pro	Ala	Thr	Thr	Phe	Gln	Ala	Phe	Gln	Ile	Ala	Leu
									1000					1005	
995															
agt	tgg	att	gca	gcc	ttg	ttg	gta	aag	caa	att	ctt	agc	cac	aaa	gaa
Ser	Trp	Ile	Ala	Ala	Leu	Leu	Val	Lys	Gln	Ile	Leu	Ser	His	Lys	Glu
									1010					1020	
1010															
tct	ctg	gtc	cgt	gca	aat	tct	gaa	tta	gct	ttc	aaa	tgc	tct	aga	gta
Ser	Leu	Val	Arg	Ala	Asn	Ser	Glu	Leu	Ala	Phe	Lys	Cys	Ser	Arg	Val
									1025					1035	
1025															
gag	gtg	gat	tat	att	tat	tcg	ata	ttg	tcc	tgc	atg	aag	agt	ctg	ttc
Glu	Val	Asp	Tyr	Ile	Tyr	Ser	Ile	Leu	Ser	Cys	Met	Lys	Ser	Leu	Phe
									1040					1050	
1040															
ctg	gag	cat	aca	caa	ggt	ttg	cag	ttc	gat	tgc	ttt	ggt	act	aat	tct
Leu	Glu	His	Thr	Gln	Gly	Leu	Gln	Phe	Asp	Cys	Phe	Gly	Thr	Asn	Ser
									1060					1070	
1055															
aaa	cag	tca	gtg	gtt	agc	aca	aaa	cta	gta	aat	gaa	agt	ctc	tca	ggg
Lys	Gln	Ser	Val	Val	Ser	Thr	Lys	Leu	Val	Asn	Glu	Ser	Leu	Ser	Gly
									1075					1085	
1075															
gct	aca	gtg	cgt	gac	gaa	aag	att	aat	acg	aag	tcg	atg	cga	aat	agc
Ala	Thr	Val	Arg	Asp	Glu	Lys	Ile	Asn	Thr	Lys	Ser	Met	Arg	Asn	Ser
									1090					1100	
1090															
tca	gag	gat	gaa	gag	tgc	atg	act	gag	aag	aga	tgt	agc	cat	tat	agc
Ser	Glu	Asp	Glu	Glu	Cys	Met	Thr	Glu	Lys	Arg	Cys	Ser	His	Tyr	Ser
									1105					1115	
1105															
aca	gca	aca	aga	gat	atc	gaa	aag	act	att	agt	ggc	ata	aaa	aag	aaa
Thr	Ala	Thr	Arg	Asp	Ile	Glu	Lys	Thr	Ile	Ser	Gly	Ile	Lys	Lys	Lys
									1120					1130	
1120															

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tac aag aag caa gtg caa aag ctt gta caa gag cat gag gaa aag aaa Tyr Lys Lys Gln Val Gln Lys Leu Val Gln Glu His Glu Glu Lys Lys 1135 1140 1145 1150					3759
atg gag ctg tta aat atg tat gca gac aag aag cag aaa ctt gaa act Met Glu Leu Leu Asn Met Tyr Ala Asp Lys Lys Gln Lys Leu Glu Thr 1155 1160 1165					3807
agt aaa agt gtg gaa gca gca gta att cgt att acc tgt tca cgg acc Ser Lys Ser Val Glu Ala Ala Val Ile Arg Ile Thr Cys Ser Arg Thr 1170 1175 1180					3855
agt act caa gtg ggt gat ctc aaa ctg ctg gat cat aat tat gaa aga Ser Thr Gln Val Gly Asp Leu Lys Leu Asp His Asn Tyr Glu Arg 1185 1190 1195					3903
aag ttt gat gaa atc aaa agt gag aaa aat gaa tgc ctc aaa agt ctg Lys Phe Asp Glu Ile Lys Ser Glu Lys Asn Glu Cys Leu Lys Ser Leu 1200 1205 1210					3951
gag caa atg cac gag gtt gca aag aag aag ttg gct gag gat gaa gcc Glu Gln Met His Glu Val Ala Lys Lys Lys Leu Ala Glu Asp Glu Ala 1215 1220 1225 1230					3999
tgt tgg att aat cggtata aag agc tgg gca gct aaa tta aaa gtt tgt Cys Trp Ile Asn Arg Ile Lys Ser Trp Ala Ala Lys Leu Lys Val Cys 1235 1240 1245					4047
gtt ccc att caa agt ggc aat aac aag cat ttt agt ggt tca tca aac Val Pro Ile Gln Ser Gly Asn Asn Lys His Phe Ser Gly Ser Ser Asn 1250 1255 1260					4095
att tcc caa aat gct cct gat gta caa att tgc aat aat gct aac gtt Ile Ser Gln Asn Ala Pro Asp Val Gln Ile Cys Asn Asn Ala Asn Val 1265 1270 1275					4143
gaa gct act tac gct gat acg aat tgc atg gct tcc aag gtt aat caa Glu Ala Thr Tyr Ala Asp Thr Asn Cys Met Ala Ser Lys Val Asn Gln 1280 1285 1290					4191
gtg cca gaa gca gaa aac aca tta gga acc atg tcg ggt ggc agc act Val Pro Glu Ala Glu Asn Thr Leu Gly Thr Met Ser Gly Gly Ser Thr 1295 1300 1305 1310					4239
caa caa gtt cat gaa atg gtg gat gta aga aat gac gag aca atg gat Gln Gln Val His Glu Met Val Asp Val Arg Asn Asp Glu Thr Met Asp 1315 1320 1325					4287
gtc tca gct ttg tct cgt gaa cag ctt aca aag agc cag tcc aat gag Val Ser Ala Leu Ser Arg Glu Gln Leu Thr Lys Ser Gln Ser Asn Glu 1330 1335 1340					4335
cac gct tct atc act gtg cct gag att ttg att cct gct gac tgt caa His Ala Ser Ile Thr Val Pro Glu Ile Leu Ile Pro Ala Asp Cys Gln 1345 1350 1355					4383
gag gaa ttt gcg gcc ttg aac gtg cat ttg tca gaa gac cag aat tgt Glu Glu Phe Ala Ala Leu Asn Val His Leu Ser Glu Asp Gln Asn Cys 1360 1365 1370					4431
gac aga ata aca tct gcg gca tca gat gaa gat gtt tca tca agg gtg Asp Arg Ile Thr Ser Ala Ala Ser Asp Glu Asp Val Ser Ser Arg Val 1375 1380 1385 1390					4479

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cca gag gta tcc cag tca ctc gaa aat ctt tct gcc tcc ccc gag ttt Pro Glu Val Ser Gln Ser Leu Glu Asn Leu Ser Ala Ser Pro Glu Phe 1395 1400 1405	4527
tct cta aat aga gag gag gct ttg gtt aca aca gaa aat aga aga aca Ser Leu Asn Arg Glu Glu Ala Leu Val Thr Thr Glu Asn Arg Arg Thr 1410 1415 1420	4575
agt cat gtg ggt ttt gat act gat aac att ttg gac cag cag aat aga Ser His Val Gly Phe Asp Thr Asp Asn Ile Leu Asp Gln Gln Asn Arg 1425 1430 1435	4623
gaa gat tgt tct ctt gac caa gag att cct gac gag tta gcg atg cct Glu Asp Cys Ser Leu Asp Gln Glu Ile Pro Asp Glu Leu Ala Met Pro 1440 1445 1450	4671
gtg caa cat ctt gcg tct gtg gta gag act agg ggt gct gct gaa tct Val Gln His Leu Ala Ser Val Val Glu Thr Arg Gly Ala Ala Glu Ser 1455 1460 1465 1470	4719
gat cag tat ggt caa gat ata tgt cct atg cct tct tca ctg gct gga Asp Gln Tyr Gly Gln Asp Ile Cys Pro Met Pro Ser Ser Leu Ala Gly 1475 1480 1485	4767
aag caa cct gac cca gca aac act gag agc gaa aat ctt gaa gaa Lys Gln Pro Asp Pro Ala Ala Asn Thr Glu Ser Glu Asn Leu Glu Glu 1490 1495 1500	4815
gca att gag cct cag tct gct ggt tca gaa aca gta gag act act gat Ala Ile Glu Pro Gln Ser Ala Gly Ser Glu Thr Val Glu Thr Thr Asp 1505 1510 1515	4863
ttt gct gca tca cat cag ggt gat caa gtt aca tgt cct ttg cta tct Phe Ala Ala Ser His Gln Gly Asp Gln Val Thr Cys Pro Leu Leu Ser 1520 1525 1530	4911
tca ccg act gga aat cag cct gcg cca gaa gca aat att gaa ggc caa Ser Pro Thr Gly Asn Gln Pro Ala Pro Glu Ala Asn Ile Glu Gly Gln 1535 1540 1545 1550	4959
aat atc aac aca tca gct gag ccc cat gta gcg ggt cca gat gca gta Asn Ile Asn Thr Ser Ala Glu Pro His Val Ala Gly Pro Asp Ala Val 1555 1560 1565	5007
gag agt ggt gat tat gca gta ata gat cag gaa aca atg ggt gct cag Glu Ser Gly Asp Tyr Ala Val Ile Asp Gln Glu Thr Met Gly Ala Gln 1570 1575 1580	5055
gat gca tgc tct ctg cca tct gga tcg gtt gga act cag tct gac cta Asp Ala Cys Ser Leu Pro Ser Gly Ser Val Gly Thr Gln Ser Asp Leu 1585 1590 1595	5103
gga gca aac att gag ggt caa aat gtc aca aca gtg gct caa ctt ccc Gly Ala Asn Ile Glu Gly Gln Asn Val Thr Thr Val Ala Gln Leu Pro 1600 1605 1610	5151
aca gat gga tca gat gca gtt gta acc ggt gga tct cct gta tca gat Thr Asp Gly Ser Asp Ala Val Val Thr Gly Gly Ser Pro Val Ser Asp 1615 1620 1625 1630	5199
cag tgt gcc cag gat gca tct cct atg cca tta tct tcg cct gga aat Gln Cys Ala Gln Asp Ala Ser Pro Met Pro Leu Ser Ser Pro Gly Asn	5247

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1635	1640	1645	
cac cct gat aca gca gtt aat atc gag ggt tta gat aac aca tca gta His Pro Asp Thr Ala Val Asn Ile Glu Gly Leu Asp Asn Thr Ser Val 1650 1655 1660			5295
gct gag cct cat ata agt gga tca gat gca tgt gaa atg gaa att tca Ala Glu Pro His Ile Ser Gly Ser Asp Ala Cys Glu Met Glu Ile Ser 1665 1670 1675			5343
gaa cct ggt ccc caa gta gag cg ^g tca acc ttt gca aat ctt ttc cat Glu Pro Gly Pro Gln Val Glu Arg Ser Thr Phe Ala Asn Leu Phe His 1680 1685 1690			5391
gaa ggt ggc gtg gag cat tca gca ggt gta aca gct ctt gtt cca tca Glu Gly Gly Val Glu His Ser Ala Gly Val Thr Ala Leu Val Pro Ser 1695 1700 1705 1710			5439
ctt ctt aac aat ggt acg gaa cag att gcc gtt caa cct gtt cct caa Leu Leu Asn Asn Gly Thr Glu Gln Ile Ala Val Gln Pro Val Pro Gln 1715 1720 1725			5487
ata cct ttc cct gtg ttc aac gac cc ^g ttt ctg cat gaa ctg gag aag Ile Pro Phe Pro Val Phe Asn Asp Pro Phe Leu His Glu Leu Glu Lys 1730 1735 1740			5535
ttg cgg aga gaa tca gag aac tca aag aag act ttt gaa gaa aaa aaa Leu Arg Arg Glu Ser Glu Asn Ser Lys Lys Thr Phe Glu Glu Lys Lys 1745 1750 1755			5583
tca atc ttg aaa gct gaa ctc gag agg aag atg gct gaa gta caa gca Ser Ile Leu Lys Ala Glu Leu Glu Arg Lys Met Ala Glu Val Gln Ala 1760 1765 1770			5631
gag ttt cga aga aaa ttt cat gag gta gaa gcc gag cat aac acc aga Glu Phe Arg Arg Lys Phe His Glu Val Glu Ala Glu His Asn Thr Arg 1775 1780 1785 1790			5679
acg aca aag ata gag aag gat aag aat ctt gtt ata atg aac aaa ctg Thr Thr Lys Ile Glu Lys Asp Lys Asn Leu Val Ile Met Asn Lys Leu 1795 1800 1805			5727
ttg gcg aat gcg ttc ttg tcc aaa tgt act gac aag aag gta tct ccc Leu Ala Asn Ala Phe Leu Ser Lys Cys Thr Asp Lys Lys Val Ser Pro 1810 1815 1820			5775
tca gga gct cca agg ggt aaa att cag cag cta gca cag aga gca gca Ser Gly Ala Pro Arg Gly Lys Ile Gln Gln Leu Ala Gln Arg Ala Ala 1825 1830 1835			5823
caa gtg agt gca ctg aga aat tac att gct cct cag cag ctt cag gca Gln Val Ser Ala Leu Arg Asn Tyr Ile Ala Pro Gln Gln Leu Gln Ala 1840 1845 1850			5871
tct tct ttt cct gct cct gct ctg gtt tcg gct cct ctg caa ctt cag Ser Ser Phe Pro Ala Pro Ala Leu Val Ser Ala Pro Leu Gln Leu Gln 1855 1860 1865 1870			5919
caa tca tca ttt cct gct cct ggt cc ^g gct cct ctg cag cct cag gca Gln Ser Ser Phe Pro Ala Pro Gly Pro Ala Pro Leu Gln Pro Gln Ala 1875 1880 1885			5967
tct tcg ttt cct tct tca gtc tct cgt cca tca gcc ctt ctt ctg aat			6015

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<210> 3
<211> 2001
<212> PRT
<213> *Arabidopsis thaliana*

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Ser Lys Gly Ser Asp Asn Ser Ile Arg Lys Gly Asp Thr Ser Pro Asp
100 105 110

Ile Glu Gln Arg Lys Asp Ser Val Glu Glu Ser Thr Asp Lys Ile Lys
115 120 125

Pro Ile Met Ser Ala Arg Ser Tyr Arg Ala Leu Phe Arg Gly Lys Leu
130 135 140

Lys Glu Ser Glu Ala Leu Val Asp Ala Ser Pro Asn Glu Glu Glu Leu
145 150 155 160

Val Val Val Gly Cys Ser Arg Arg Ile Pro Ala Gly Asn Asp Asp Val
165 170 175

Gln Gly Lys Thr Asp Cys Pro Pro Pro Ala Asp Ala Gly Ser Lys Arg
180 185 190

Leu Pro Val Asp Glu Thr Ser Leu Asp Lys Gly Thr Asp Phe Pro Leu
195 200 205

Lys Ser Val Thr Glu Thr Glu Lys Ile Val Leu Asp Ala Ser Pro Ile
210 215 220

Val Glu Thr Gly Asp Asp Ser Val Ile Gly Ser Pro Ser Glu Asn Leu
225 230 235 240

Glu Thr Gln Lys Leu Gln Asp Gly Lys Thr Asp Cys Ser Pro Pro Ala
245 250 255

Asn Ala Glu Ser Lys Thr Leu Pro Val Gly Glu Thr Ser Leu Glu Lys
260 265 270

Glu Tyr Pro Gln Lys Phe Gln Asp Asp Asn Thr Asp Cys Leu Pro Pro
275 280 285

Ala Asn Ala Glu Ser Lys Arg Leu Pro Val Gly Glu Thr Ser Leu Glu
290 295 300

Lys Asp Thr Asp Phe Pro Leu Lys Ser Thr Thr Glu Thr Gly Lys Met
305 310 315 320

Val Leu Tyr Ala Ser Pro Ile Val Glu Thr Arg Asp Asp Ser Val Ile
325 330 335

Cys Ser Pro Ser Thr Asn Leu Glu Thr Gln Lys Leu Leu Val Ser Lys
340 345 350

Thr Gly Leu Glu Thr Asp Ile Val Leu Pro Leu Lys Arg Lys Arg Asp
355 360 365

Thr Ala Glu Ile Glu Leu Asp Ala Cys Ala Thr Val Ala Asn Gly Asp
370 375 380

Asp His Val Met Ser Ser Asp Gly Val Ile Pro Ser Pro Ser Gly Cys
385 390 395 400

Lys Asn Asp Asn Arg Pro Glu Met Cys Asn Thr Cys Lys Lys Arg Gln
405 410 415

Lys Val Asn Gly Asp Cys Gln Asn Arg Ser Val Cys Ser Cys Ile Val
420 425 430

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Gln Pro Val Glu Glu Ser Asp Asn Val Thr Gln Asp Met Lys Glu Thr
435 440 445

Gly Pro Val Thr Ser Arg Glu Tyr Glu Glu Asn Gly Gln Ile Gln His
450 455 460

Gly Lys Ser Ser Asp Pro Lys Phe Tyr Ser Ser Val Tyr Pro Glu Tyr
465 470 475 480

Trp Val Pro Val Gln Leu Ser Asp Val Gln Leu Glu Gln Tyr Cys Gln
485 490 495

Thr Leu Phe Ser Lys Ser Leu Ser Leu Ser Ser Leu Ser Lys Ile Asp
500 505 510

Leu Gly Ala Leu Glu Glu Thr Leu Asn Ser Val Arg Lys Thr Cys Asp
515 520 525

His Pro Tyr Val Met Asp Ala Ser Leu Lys Gln Leu Leu Thr Lys Asn
530 535 540

Leu Glu Leu His Glu Ile Leu Asp Val Glu Ile Lys Ala Ser Gly Lys
545 550 555 560

Leu His Leu Leu Asp Lys Met Leu Thr His Ile Lys Lys Asn Gly Leu
565 570 575

Lys Ala Val Val Phe Tyr Gln Ala Thr Gln Thr Pro Glu Gly Leu Leu
580 585 590

Leu Gly Asn Ile Leu Glu Asp Phe Val Gly Gln Arg Phe Gly Pro Lys
595 600 605

Ser Tyr Glu His Gly Ile Tyr Ser Ser Lys Lys Asn Ser Ala Ile Asn
610 615 620

Asn Phe Asn Lys Glu Ser Gln Cys Cys Val Leu Leu Leu Glu Thr Arg
625 630 635 640

Ala Cys Ser Gln Thr Ile Lys Leu Leu Arg Ala Asp Ala Phe Ile Leu
645 650 655

Phe Gly Ser Ser Leu Asn Pro Ser His Asp Val Lys His Val Glu Lys
660 665 670

Ile Lys Ile Glu Ser Cys Ser Glu Arg Thr Lys Ile Phe Arg Leu Tyr
675 680 685

Ser Val Cys Thr Val Glu Glu Lys Ala Leu Ile Leu Ala Arg Gln Asn
690 695 700

Met Arg Gln Asn Lys Ala Val Glu Asn Leu Asn Arg Ser Leu Thr His
705 710 715 720

Ala Leu Leu Met Trp Gly Ala Ser Tyr Leu Phe Asp Lys Leu Asp His
725 730 735

Phe His Ser Ser Glu Thr Pro Asp Ser Gly Val Ser Phe Glu Gln Ser
740 745 750

Ile Met Asp Gly Val Ile His Glu Phe Ser Ser Ile Leu Ser Ser Lys
755 760 765

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Gly Gly Glu Glu Asn Glu Val Lys Leu Cys Leu Leu Glu Ala Lys
770 775 780

His Ala Gln Gly Thr Tyr Ser Ser Asp Ser Thr Leu Phe Gly Glu Asp
785 790 795 800

His Ile Lys Leu Ser Asp Glu Glu Ser Pro Asn Ile Phe Trp Ser Lys
805 810 815

Leu Leu Gly Gly Lys Asn Pro Met Trp Lys Tyr Pro Ser Asp Thr Pro
820 825 830

Gln Arg Asn Arg Lys Arg Val Gln Tyr Phe Glu Gly Ser Glu Ala Ser
835 840 845

Pro Lys Thr Gly Asp Gly Gly Asn Ala Lys Lys Arg Lys Lys Ala Ser
850 855 860

Asp Asp Val Thr Asp Pro Arg Val Thr Asp Pro Pro Val Asp Asp Asp
865 870 875 880

Glu Arg Lys Ala Ser Gly Lys Asp His Met Gly Ala Leu Glu Ser Pro
885 890 895

Lys Val Ile Thr Leu Gln Ser Ser Cys Lys Ser Ser Gly Thr Asp Gly
900 905 910

Thr Leu Asp Gly Asn Asp Ala Phe Gly Leu Tyr Ser Met Gly Ser His
915 920 925

Ile Ser Gly Ile Pro Glu Asp Met Leu Ala Ser Gln Asp Trp Gly Lys
930 935 940

Ile Pro Asp Glu Ser Gln Arg Arg Leu His Thr Val Leu Lys Pro Lys
945 950 955 960

Met Ala Lys Leu Cys Gln Val Leu His Leu Ser Asp Ala Cys Thr Ser
965 970 975

Met Val Gly Asn Phe Leu Glu Tyr Val Ile Glu Asn His Arg Ile Tyr
980 985 990

Glu Glu Pro Ala Thr Thr Phe Gln Ala Phe Gln Ile Ala Leu Ser Trp
995 1000 1005

Ile Ala Ala Leu Leu Val Lys Gln Ile Leu Ser His Lys Glu Ser
1010 1015 1020

Leu Val Arg Ala Asn Ser Glu Leu Ala Phe Lys Cys Ser Arg Val
1025 1030 1035

Glu Val Asp Tyr Ile Tyr Ser Ile Leu Ser Cys Met Lys Ser Leu
1040 1045 1050

Phe Leu Glu His Thr Gln Gly Leu Gln Phe Asp Cys Phe Gly Thr
1055 1060 1065

Asn Ser Lys Gln Ser Val Val Ser Thr Lys Leu Val Asn Glu Ser
1070 1075 1080

Leu Ser Gly Ala Thr Val Arg Asp Glu Lys Ile Asn Thr Lys Ser
1085 1090 1095

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Met	Arg	Asn	Ser	Ser	Glu	Asp	Glu	Glu	Cys	Met	Thr	Glu	Lys	Arg
1100					1105					1110				
Cys	Ser	His	Tyr	Ser	Thr	Ala	Thr	Arg	Asp	Ile	Glu	Lys	Thr	Ile
1115					1120					1125				
Ser	Gly	Ile	Lys	Lys	Lys	Tyr	Lys	Lys	Gln	Val	Gln	Lys	Leu	Val
1130					1135					1140				
Gln	Glu	His	Glu	Glu	Lys	Lys	Met	Glu	Leu	Leu	Asn	Met	Tyr	Ala
1145					1150						1155			
Asp	Lys	Lys	Gln	Lys	Leu	Glu	Thr	Ser	Lys	Ser	Val	Glu	Ala	Ala
1160					1165						1170			
Val	Ile	Arg	Ile	Thr	Cys	Ser	Arg	Thr	Ser	Thr	Gln	Val	Gly	Asp
1175					1180						1185			
Leu	Lys	Leu	Leu	Asp	His	Asn	Tyr	Glu	Arg	Lys	Phe	Asp	Glu	Ile
1190					1195						1200			
Lys	Ser	Glu	Lys	Asn	Glu	Cys	Leu	Lys	Ser	Leu	Glu	Gln	Met	His
1205					1210						1215			
Glu	Val	Ala	Lys	Lys	Lys	Leu	Ala	Glu	Asp	Glu	Ala	Cys	Trp	Ile
1220					1225						1230			
Asn	Arg	Ile	Lys	Ser	Trp	Ala	Ala	Lys	Leu	Lys	Val	Cys	Val	Pro
1235					1240						1245			
Ile	Gln	Ser	Gly	Asn	Asn	Lys	His	Phe	Ser	Gly	Ser	Ser	Asn	Ile
1250					1255						1260			
Ser	Gln	Asn	Ala	Pro	Asp	Val	Gln	Ile	Cys	Asn	Asn	Ala	Asn	Val
1265					1270						1275			
Glu	Ala	Thr	Tyr	Ala	Asp	Thr	Asn	Cys	Met	Ala	Ser	Lys	Val	Asn
1280					1285						1290			
Gln	Val	Pro	Glu	Ala	Glu	Asn	Thr	Leu	Gly	Thr	Met	Ser	Gly	Gly
1295					1300						1305			
Ser	Thr	Gln	Gln	Val	His	Glu	Met	Val	Asp	Val	Arg	Asn	Asp	Glu
1310					1315						1320			
Thr	Met	Asp	Val	Ser	Ala	Leu	Ser	Arg	Glu	Gln	Leu	Thr	Lys	Ser
1325					1330						1335			
Gln	Ser	Asn	Glu	His	Ala	Ser	Ile	Thr	Val	Pro	Glu	Ile	Leu	Ile
1340					1345						1350			
Pro	Ala	Asp	Cys	Gln	Glu	Glu	Phe	Ala	Ala	Leu	Asn	Val	His	Leu
1355					1360						1365			
Ser	Glu	Asp	Gln	Asn	Cys	Asp	Arg	Ile	Thr	Ser	Ala	Ala	Ser	Asp
1370					1375						1380			
Glu	Asp	Val	Ser	Ser	Arg	Val	Pro	Glu	Val	Ser	Gln	Ser	Leu	Glu
1385					1390						1395			
Asn	Leu	Ser	Ala	Ser	Pro	Glu	Phe	Ser	Leu	Asn	Arg	Glu	Glu	Ala
1400					1405						1410			

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Leu	Val	Thr	Thr	Glu	Asn	Arg	Arg	Thr	Ser	His	Val	Gly	Phe	Asp
1415						1420					1425			
Thr	Asp	Asn	Ile	Leu	Asp	Gln	Gln	Asn	Arg	Glu	Asp	Cys	Ser	Leu
1430						1435					1440			
Asp	Gln	Glu	Ile	Pro	Asp	Glu	Leu	Ala	Met	Pro	Val	Gln	His	Leu
1445						1450					1455			
Ala	Ser	Val	Val	Glu	Thr	Arg	Gly	Ala	Ala	Glu	Ser	Asp	Gln	Tyr
1460						1465					1470			
Gly	Gln	Asp	Ile	Cys	Pro	Met	Pro	Ser	Ser	Leu	Ala	Gly	Lys	Gln
1475						1480					1485			
Pro	Asp	Pro	Ala	Ala	Asn	Thr	Glu	Ser	Glu	Asn	Leu	Glu	Glu	Ala
1490						1495					1500			
Ile	Glu	Pro	Gln	Ser	Ala	Gly	Ser	Glu	Thr	Val	Glu	Thr	Thr	Asp
1505						1510					1515			
Phe	Ala	Ala	Ser	His	Gln	Gly	Asp	Gln	Val	Thr	Cys	Pro	Leu	Leu
1520						1525					1530			
Ser	Ser	Pro	Thr	Gly	Asn	Gln	Pro	Ala	Pro	Glu	Ala	Asn	Ile	Glu
1535						1540					1545			
Gly	Gln	Asn	Ile	Asn	Thr	Ser	Ala	Glu	Pro	His	Val	Ala	Gly	Pro
1550						1555					1560			
Asp	Ala	Val	Glu	Ser	Gly	Asp	Tyr	Ala	Val	Ile	Asp	Gln	Glu	Thr
1565						1570					1575			
Met	Gly	Ala	Gln	Asp	Ala	Cys	Ser	Leu	Pro	Ser	Gly	Ser	Val	Gly
1580						1585					1590			
Thr	Gln	Ser	Asp	Leu	Gly	Ala	Asn	Ile	Glu	Gly	Gln	Asn	Val	Thr
1595						1600					1605			
Thr	Val	Ala	Gln	Leu	Pro	Thr	Asp	Gly	Ser	Asp	Ala	Val	Val	Thr
1610						1615					1620			
Gly	Gly	Ser	Pro	Val	Ser	Asp	Gln	Cys	Ala	Gln	Asp	Ala	Ser	Pro
1625						1630					1635			
Met	Pro	Leu	Ser	Ser	Pro	Gly	Asn	His	Pro	Asp	Thr	Ala	Val	Asn
1640						1645					1650			
Ile	Glu	Gly	Leu	Asp	Asn	Thr	Ser	Val	Ala	Glu	Pro	His	Ile	Ser
1655						1660					1665			
Gly	Ser	Asp	Ala	Cys	Glu	Met	Glu	Ile	Ser	Glu	Pro	Gly	Pro	Gln
1670						1675					1680			
Val	Glu	Arg	Ser	Thr	Phe	Ala	Asn	Leu	Phe	His	Glu	Gly	Gly	Val
1685						1690					1695			
Glu	His	Ser	Ala	Gly	Val	Thr	Ala	Leu	Val	Pro	Ser	Leu	Leu	Asn
1700						1705					1710			
Asn	Gly	Thr	Glu	Gln	Ile	Ala	Val	Gln	Pro	Val	Pro	Gln	Ile	Pro
1715						1720					1725			

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Phe	Pro	Val	Phe	Asn	Asp	Pro	Phe	Leu	His	Glu	Leu	Glu	Lys	Leu
1730						1735					1740			
Arg	Arg	Glu	Ser	Glu	Asn	Ser	Lys	Lys	Thr	Phe	Glu	Glu	Lys	Lys
1745						1750					1755			
Ser	Ile	Leu	Lys	Ala	Glu	Leu	Glu	Arg	Lys	Met	Ala	Glu	Val	Gln
1760						1765					1770			
Ala	Glu	Phe	Arg	Arg	Lys	Phe	His	Glu	Val	Glu	Ala	Glu	His	Asn
1775						1780					1785			
Thr	Arg	Thr	Thr	Lys	Ile	Glu	Lys	Asp	Lys	Asn	Leu	Val	Ile	Met
1790						1795					1800			
Asn	Lys	Leu	Leu	Ala	Asn	Ala	Phe	Leu	Ser	Lys	Cys	Thr	Asp	Lys
1805						1810					1815			
Lys	Val	Ser	Pro	Ser	Gly	Ala	Pro	Arg	Gly	Lys	Ile	Gln	Gln	Leu
1820						1825					1830			
Ala	Gln	Arg	Ala	Ala	Gln	Val	Ser	Ala	Leu	Arg	Asn	Tyr	Ile	Ala
1835						1840					1845			
Pro	Gln	Gln	Leu	Gln	Ala	Ser	Ser	Phe	Pro	Ala	Leu	Val		
1850						1855					1860			
Ser	Ala	Pro	Leu	Gln	Leu	Gln	Gln	Ser	Ser	Phe	Pro	Ala	Pro	Gly
1865						1870					1875			
Pro	Ala	Pro	Leu	Gln	Pro	Gln	Ala	Ser	Ser	Phe	Pro	Ser	Ser	Val
1880						1885					1890			
Ser	Arg	Pro	Ser	Ala	Leu	Leu	Leu	Asn	Phe	Ala	Val	Cys	Pro	Met
1895						1900					1905			
Pro	Gln	Pro	Arg	Gln	Pro	Leu	Ile	Ser	Asn	Ile	Ala	Pro	Thr	Pro
1910						1915					1920			
Ser	Val	Thr	Pro	Ala	Thr	Asn	Pro	Gly	Leu	Arg	Ser	Pro	Ala	Pro
1925						1930					1935			
His	Leu	Asn	Ser	Tyr	Arg	Pro	Ser	Ser	Ser	Thr	Pro	Val	Ala	Thr
1940						1945					1950			
Ala	Thr	Pro	Thr	Ser	Ser	Val	Pro	Pro	Gln	Ala	Leu	Thr	Tyr	Ser
1955						1960					1965			
Ala	Val	Ser	Ile	Gln	Gln	Gln	Gln	Glu	Gln	Gln	Pro	Gln	Gln	Ser
1970						1975					1980			
Leu	Ser	Ser	Gly	Leu	Gln	Ser	Asn	Asn	Glu	Val	Val	Cys	Leu	Ser
1985						1990					1995			
Asp	Asp	Glu												

<210> 4
<211> 21
<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Oligonucleotide

<400> 4
catctacggc aatgtaccag c

21

<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Oligonucleotide

<400> 5
gatgggaatt ggctgagtgg c

21

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Oligonucleotide

<400> 6
cagttccaaa cgtaaaacgg c

21

<210> 7
<211> 15
<212> DNA
<213> Artificial Sequence

<220>

<222> 1

<223> Description of Artificial Sequence: Synthetic Oligonucleotide
n= a, t, g, or c

<400> 7
ntcgastwts gwgtt

15

<210> 8
<211> 16
<212> DNA
<213> Artificial Sequence

<220>

<222> 1

<223> Description of Artificial Sequence: Synthetic Oligonucleotide
n= a, t, g, or c

<400> 8

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16

ngtcgaswga nawgaa

<210> 9
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<222> 5..13
<223> Description of Artificial Sequence:Synthetic Oligonucleotide
n= a, t, g, or c

<400> 9
wgtgnagwan canaga

16

<210> 10
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<222> 6..13
<223> Description of Artificial Sequence:Synthetic Oligonucleotide
n= a, t, g, or c

<400> 10
wggwancwga wangca

16

<210> 11
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<222> 11..13
<223> Description of Artificial Sequence:Synthetic Oligonucleotide
n= a, t, g, or c

<400> 11
wcgwwgawca ngncga

16

<210> 12
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<222> 4..13
<223> Description of Artificial Sequence:Synthetic Oligonucleotide
n= a, t, g, or c

<400> 12
wgcnagtnag wanaag

16

Third Corrected Sequence Listing 5-2002

<210> 13
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<222> 6..13
<223> Description of Artificial Sequence:Synthetic Oligonucleotide
n= a, t, g, or c

<400> 13
awgcangncw ganata 16

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<222> 1..24
<223> Description of Artificial Sequence:Synthetic Oligonucleotide

<400> 14
ctgtacatac tgagtacaat cgga 24

<210> 15
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<222> 1..25
<223> Description of Artificial Sequence:Synthetic Oligonucleotide

<400> 15
gcttcaattc ctgcctcagt tgaac 25

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<222> 1..24
<223> Description of Artificial Sequence:Synthetic Oligonucleotide

<400> 16
ctctacgtgc ttaacatcat gcga 24

<210> 17
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

Third Corrected Sequence Listing 5-2002

<222> 1..25
<223> Description of Artificial Sequence:synthetic
Oligonucleotide

<400> 17
ccagttctg ctactagaaa gtcag 25

<210> 18
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<222> 1..25
<223> Description of Artificial Sequence:synthetic
Oligonucleotide

<400> 18
ctggagttgc atgaaatcct ggatg 25

<210> 19
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<222> 1..25
<223> Description of Artificial Sequence: Synthetic
Oligonucleotide

<400> 19
gctcttgta agctgttac gagac 25

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<222> 1..24
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 20
tcgcatgatg ttaaggcacgt agag 24

<210> 21
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<222> 1..25
<223> Description of Artificial Sequence:Synthetic
Oligonucleotide

<400> 21
gagtactggc ccgtgaacag gtaat 25

Third Corrected Sequence Listing 5-2002

<210> 22
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<222> 1..25
<223> Description of Artificial Sequence:Synthetic Oligonucleotide

<400> 22 atgcttgcac aagcatggtc ggaaa 25

<210> 23
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<222> 1..25
<223> Description of Artificial Sequence:Synthetic Oligonucleotide

<400> 23 tgcaacatcg tgcatttgct ccaga 25

<210> 24
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<222> 1..25
<223> Description of Artificial Sequence:Synthetic Oligonucleotide

<400> 24 cacaaggcatg agttttcct tccgg 25

<210> 25
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<222> 1..25
<223> Description of Artificial Sequence:Synthetic Oligonucleotide

<400> 25 ctgactttct agtagcagaa gctgg 25

<210> 26
<211> 519
<212> DNA
<213> Brassica oleracea

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<220>

<222> 10..11

<223> seq1-23

n= a, t, g, or c

<400> 26

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tccactcccc	tggaagtgtt	ccagcttatac	aaataaaatataat	gatgcccccc	acatgagcaa	120
tgcatgtgt	agaggacggt	ttaggttctc	tagaggctta	tttgcctag	caagaatcag	180
ggtttttct	tcaactgtaa	acactgagta	caaccggaaa	atcttagttc	tttcagaaca	240
cgactcaacc	tttatcttct	ctaagagctt	aacgtcatgc	gatggattca	ggctgctcc	300
aaaaagtata	aaagactcag	cgcgtaaagag	ttaatgctt	tgactacagg	cacgtatttc	360
cagcagcaga	ataaaaacact	cactctcctt	gttgaatttg	tttatacgct	tcttcttcga	420
gaggcagacc	ccatgctcat	aggaattttg	accaaatttt	tgcatcagaa	aatcttcgag	480
aatattacca	agcagaagcc	cctcaggcgt	atgtatttc			519

<210> 27

<211> 419

<212> DNA

<213> Brassica oleracea

<220>

<223> seq1-27

<400> 27

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tcctgtggaa	gtactaagg	atatacgaa	gacagtgggt	gattcatccc	ccatgggtga	120
aactgaggat	ggcagtgtta	taggttccacc	atccgagaat	ccagaaccac	aaaagcttcg	180
tgacagtgaa	actagcttgg	aaaccgatata	agacttgct	ctgaaaagaa	aaagagacac	240
tgcagaaaatt	gtgatggatg	catgtacaaa	tgcagatgac	cgcattatga	gtactgatgg	300
gtttattccct	tttccaccccg	tgtgcacaaa	tattaatcaa	ccgaaaggt	gtggcacatg	360
tcaaaaacgg	caaaagttaag	aatttccgac	tgttgcgtgt	cgtttgaaa	ccatttgcc	419

<210> 28

<211> 467

<212> DNA

<213> Brassica oleracea

<220>

<223> seq1-43

<400> 28

gaattctcg	ccatactttc	ttccgatgtt	ggagaagaaaa	atgaaggcaa	gctgtgtcta	60
cttttggaa	ccaagcatgc	tcagggaaat	tacagcactg	atgtctactt	atttgggtgaa	120
gaacatgtca	agttatcaga	tgaagatcca	aatatgtttt	ggtcaaagct	gttgagtgaa	180
aagaacccta	tgtggaaata	ctgttcggat	actcctcaaa	ggagtcgaaa	aagagtacgg	240
catcttcagg	gttatgagga	gactacaaa	gttggcaatg	gcggaaactt	aaagaagaaa	300
aagaaggctt	cagatgtat	cacagtat	aacgctgaga	gaaaagcctc	tggaaaggat	360
cacatgggta	aaacagttca	cttcctgctc	ctttaacctt	agtgttcatt	gaatgttcca	420
tttactttgc	ttactatctt	tccttcaggg	catttggagt	caccaaa		467

<210> 29

<211> 490

<212> DNA

<213> Brassica oleracea

<220>

<223> seq1-47

<400> 29

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gaattcagct	ttaaaaactg	atctctgctc	acagataatt	taagagttag	tgaaaattga	60
gataaaaacga	accaaaaactg	gaggtaacag	atactctgag	aacaactaac	cttttcttca	120
taagtcttct	ttgtgttctc	tgattctctc	cgcagcttct	ccagttcatg	ctgaaatggg	180
tcactgaaca	cagggaaagg	tacttgagga	acaggtggag	tggcattctg	tcccgttagca	240
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<212> DNA

<213> Brassica oleracea

<220>

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tgtactttt	aaagaaaagg	tgtatgatctc	aaaggagagt	tggatgaatg	ccttgaagt	420
ttagagcaaa	taaacgaggc	tggaaagaag	aagttggctg	aagatgaagc	ctgttggatt	480
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<212> DNA

<213> Brassica oleracea

<220>

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tcgacaacag	ttgttcttt	ataacaagat	tcttcctcg	ctgtacttc	gtcttctgg	480
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<212> DNA

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<223> seq2-53

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Third Corrected Sequence Listing 5-2002

tggtttcttc	ttgcttact	ttggacacct	gtttaatatt	ggccgtcaa	atttacttat	180
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<220>
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<223> ATP/GTP-binding motif A concensus sequence

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<222> 2..5
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<223> Xaa= Ser or Thr

<400> 34
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1 5